

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 16, 2003, 16:37:55 : Search time 1447.31 Seconds  
(without alignments)  
15778.007 Million cell updates/sec

Title: US-09-497-967-44  
Perfect score: 1410  
Sequence: 1 atgaaaaataatttttagt.....cttattattattatgatga 1410

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues  
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_nam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	208.6	14.8	658	14 BQ135057	BQ135057 INIT1_2_G
C 2	205.2	14.6	607	14 BQ134912	BQ134912 INIT1_1_F
C 3	198	14.0	602	14 BQ135164	BQ135164 INIT1_4_B
C 4	197	14.0	590	14 BQ135179	BQ135179 INIT1_4_C
C 5	171	12.1	502	14 BQ134889	BQ134889 INIT1_1_D
C 6	163	11.6	445	14 BQ134871	BQ134871 INIT1_1_B

C 7	156.8	11.1	419	14 BQ135036	BQ135036 INIT1_2_D
C 8	134.4	9.5	675	14 BQ135196	BQ135196 INIT1_4_E
C 9	127.8	9.1	599	14 BQ134821	BQ134821 INIT1_4_D
10	115.2	8.2	540	14 BQ134879	BQ134879 INIT1_1_C
11	113.8	8.1	538	14 BQ134810	BQ134810 INIT1_4_C
12	110.4	7.8	630	14 BQ134905	BQ134905 INIT1_1_F
13	110.4	7.8	631	14 BQ134827	BQ134827 INIT1_4_E
14	109.4	7.8	523	14 BQ134970	BQ134970 INIT1_2_D
C 15	108.6	7.7	337	14 BQ134748	BQ134748 INIT1_3_E
C 16	106.4	7.5	514	14 BQ134761	BQ134761 INIT1_3_F
17	106.4	7.5	661	14 BQ135189	BQ135189 INIT1_4_D
18	105.8	7.5	560	14 BQ135129	BQ135129 INIT1_3_F
19	105.8	7.5	622	14 BQ134798	BQ134798 INIT1_4_B
20	105.8	7.5	687	14 BQ135168	BQ135168 INIT1_2_G
C 21	99.2	7.0	592	14 BQ134985	BQ134985 INIT1_1_E
C 22	72.2	5.1	210	14 BQ134900	BQ134900 INIT1_1_E
C 23	69.8	5.0	150	14 BQ135114	BQ135114 INIT1_3_E
24	68.4	4.9	773	17 CNS01VTC	AL169549 Tetraodon
C 25	62	4.4	735	17 CNS04NSM	AL299119 Tetraodon
C 26	61.4	4.4	470	17 FR0018463	AL011359 F.rubripe
27	61.4	4.4	989	17 CNS02HA4	AL197365 Tetraodon
28	61.4	4.4	1101	17 CNS0039G	AL063921 Drosophila
29	60.8	4.3	501	17 FR0048173	AL444958 Fugu rubr
C 30	58.4	4.1	605	17 AZ640388	AZ640388 1M0502E21
C 31	57.8	4.1	813	13 BJ406459	BJ406459 BJ406459
C 32	56.2	4.0	494	17 FR0048073	AL444858 Fugu rubr
C 33	56.2	4.0	572	17 CNS043SN	AL273200 Tetraodon
C 34	56.2	4.0	723	17 BH182027	BH182027 020_K_19-
C 35	56.2	4.0	723	17 CNS07NIN	AL618977 T3 end of
C 36	56	4.0	824	17 AZ185454	AZ185454 SP.1005_A
37	56	4.0	898	17 CNS04ALV	AL282028 Tetraodon
38	55.6	3.9	450	17 FR0025683	AL018519 F.rubripe
39	55.4	3.9	623	9 AU060774	AU060774 AU060774
40	55.4	3.9	742	9 AU060168	AU060168 AU060168
41	55	3.9	619	17 PR0006944	290754 F.rubripes
C 42	55	3.9	805	17 CNS04RW2	AL304427 Tetraodon
C 43	55	3.9	857	13 BJ403229	BJ403229 BJ403229
C 44	55	3.9	1101	17 CNS0039G	AL063921 Drosophila
C 45	54.8	3.9	550	17 FR0043207	AL130699 Fugu rubr

## ALIGNMENTS

RESULT 1  
BQ135057/c  
LOCUS  
DEFINITION  
BQ135057 658 bp mRNA linear EST 22-APR-2002  
INIT1\_2\_G01.g1\_A006 G5 trophont cDNA (INIT1) Ichthyophthirius  
multifiliis cDNA, mRNA sequence.  
ACCESSION  
BQ135057  
VERSION  
BQ135057.1 GI:20261156  
KEYWORDS  
EST.  
SOURCE  
Ichthyophthirius multifiliis.  
ORGANISM  
Ichthyophthirius multifiliis  
Eukaryota; Alveolata; Ciliophora; Oligophymenophorea;  
Hymenostomatida; Ophryoglenina; Ichthyophthirius.  
REFERENCE  
1 (bases 1 to 658)  
AUTHORS  
Clark, R., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A.,  
Dickerson, H., Lin, T.-L. and Pratt, L.H.  
TITLE  
An EST database for Ichthyophthirius multifiliis (G5 isolate)  
JOURNAL  
Unpublished (2002)  
COMMENT  
Contact: Cordonnier-Pratt MM  
Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmpratt@uga.edu  
Sequences have been trimmed to exclude PolyA, vector, and regions  
below Phred quality 16. The threshold for highest quality sequence  
is 20.  
Seq primer: T7  
High quality sequence start: 67

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High quality sequence stop: 658
POLYA-No.      Location/Qualifiers
1. .658
/organism="Ichthyophthirius multifiliis"
/strain="G5"
/db_xref="taxon:5932"
/clone_lib="G5 trophont cDNA (INIT1)"
/note="Vector: pBluescript SK(-) from Lambda Zap II;
Site_1: EcoRI; Site_2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.
Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into lambda ZAP
II. Plasmid DNA for sequencing was prepared by mass
excision."
BASE COUNT    215 a 122 c 122 g 199 t
ORIGIN
Query Match      14.8%; Score 208.6; DB 14; Length 658;
Best Local Similarity 65.2%; Pred. No. 2.1e-34;
Matches 393; Conservative 0; Mismatches 189; Indels 21; Gaps 5;

QY 819 TCCTAATTCATCCAGGTAATAGTACATGCTTACCTGCCAGCAATAAAGATTATGG 878
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 604 TCCTATGGTTCCCTGGCCCTAATAGTAATCGGTAGCTTCCGAATCAAAAAGACCAA--- 548

QY 879 TGTGTAGCCACTGCAGGTGGTCCGCTACTTTAGCCAAATATATGTAATTTGCATGCC 938
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 547 TCTTAATCCAGATCAGGCTTTGAGGCTAATTTAGCCGATATGTGGCAGCTGAATGCC 488

QY 939 TGATGTACTGCAATTCGTAGTGAG---CAACTAATTAATTAATAAACAAGATG 995
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 487 TGCTGCACTCTGTTACAGACGAGTAACACCTACTTATCTGATCTACTCTCAATG 428

QY 996 TCTAATTTGCTGCTAACTTTATTTGATGTAATTTCTAGCGAGGAAGTAGTAG 1055
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 427 TGTAAATGTAAAGCTGGCTTTTACT---AAATAGTAATTTTGAAGCAGGTAAGAAGTTA 371

QY 1056 ATGCAAGCATGCCAGCAATAAAGTTTAAAGCGCTGTAGCAACTGCAGGTGGTACTGC 1115
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 370 ATGCAATAAGTGTGCAGTAAGTAAGAACT---GGTTCCAGCATCTGTTCCAGGTAATAGTGC 314

QY 1116 TACTTTAATTCGAATATGTCCTTGAATGCCCTGTGTAGTGTACTCACCGATGGAAC 1175
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 313 TACTTTCAGCACATAATGTTTAAACGATTTGCCCTGTGTGTACAGTGGTGTGATGGTAC 254

QY 1176 AACATCTACTTATAAATACGACATCTGAATCTGTTAAATGTGTCACCACTTTTATAC 1235
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 253 ATCACTAATTTGTAGCTTTAGCAAGTGAATGTACTAATATGTAGCTTAACCTTTATGC 194

QY 1236 TACAAAATAACTGATTTGGGTAGCAGGTAATGATACATGTAATGTTGTAATAAAAAAT 1295
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 193 ATCAAAAACATCTGTTTTCAGCAGGTACTGATACATGTACTGTAATGTTCTAAAAAAT 134

QY 1296 AACTTCGGCGCTGAAGCTAATTTACCTGAATCTGCTAAAAAATAATATATATGTC--- 1351
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 133 AACTTCGGTGTACAGCTAAAGTATATGCTGAAGTACTTAAAAAGCATATATGCGCCAG 74

QY 1352 -----ATTTCGCTAATTTTATCAATTTCCCTTATTTATGATTTCTTATTTATG 1406
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 73 TTCACATTTTCGCAAAATTTTATCAATGCTCTTAATTTATTTCTTCTATTGTTG 14

QY 1407 ATG 1409
    |||
Db 13 ATG 11

RESULT 2
BQ134912/c      607 bp mRNA linear EST 22-APR-2002
LOCUS          INIT1.1.F12.b1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
DEFINITION     multifiliis cDNA, mRNA sequence.
ACCESSION     BQ134912

VERSION BQ134912.1 GI:20261011
KEYWORDS EST.
SOURCE Ichthyophthirius multifiliis.
ORGANISM Ichthyophthirius multifiliis
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE 1 (bases 1 to 607)
AUTHORS Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
Dickerson,H., Lin,T.-L. and Pratt,L.H.
TITLE An EST database for Ichthyophthirius multifiliis (G5 isolate)
JOURNAL Unpublished (2002)
COMMENT Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector, and regions
below phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: JEN REV
High quality sequence stop: 599
POLYA-No.      Location/Qualifiers
1. .607
/organism="Ichthyophthirius multifiliis"
/strain="G5"
/db_xref="taxon:5932"
/clone_lib="G5 trophont cDNA (INIT1)"
/note="Vector: pBluescript SK(-) from Lambda Zap II;
Site_1: EcoRI; Site_2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.
Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into lambda ZAP
II. Plasmid DNA for sequencing was prepared by mass
excision."
BASE COUNT    199 a 111 c 104 g 193 t
ORIGIN
Query Match      14.6%; Score 205.2; DB 14; Length 607;
Best Local Similarity 65.8%; Pred. No. 1.1e-33;
Matches 383; Conservative 0; Mismatches 178; Indels 21; Gaps 5;

QY 841 ACTACATGCTTACCTTGGCCAGCAATAAAGATTATGTGCTGCTGAAGCCACTGCAGGTGT 900
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 607 ACTAAATCGTAGCTTGGCAATCAAAAAGACCACAA---TTCCTTAATCCAGATCAGGTCTT 551

QY 901 GCGCTACTTTAGCCAAATAATGTAATTTGCATGCCCTGATGGTACTGCAATTTGCTAGT 960
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 550 GAGGCTAATTTAGCCGCAATAATGTGGCACTGAATGCTCTGCTGGCAGCTTTGTACAGAC 491

QY 961 GGAGCAA---CTAATATTGTAATATTATAACAGAATGCTTAATTTGCTGCTAACTTT 1017
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 490 GGAGTAACACCTTACTTATCTATCTATCTATCTCATATAATGTTAATTTGTAAGCTGGCTTT 431

QY 1018 TATTTTGATGGTAATAATTTCTAGCAGGAGTAGTAGTCAAGAGCATGTCACCAAAAT 1077
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 430 TACT---AAAATAGTAATTTTGAAGCAGGTAAGGTTAATGCAATAAGTGTGCAGTAAGT 374

QY 1078 AAAGTTTAAAGCGCTGTAGCAACTGCAGGTGGTACTGCTACTTTTAAATTTGCATAATG 1137
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 373 AAAACT---GGTTACGATCTCTTCCAGGTAATAGTGTACTTTCAGCCACATAATGTTAA 317

QY 1138 CTTGAATGCCCTGCTGCTACTGTACTACCAGTAGGAAACAATCTACTTATATAAATAGCA 1197
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 316 AACGATTTGCCCTGCTGGTACAGTGGTTGATGATGATACATCAACTAAATTTTGTAGCTTTA 257

QY 1198 GCATCTGATGTGTTAAATGTGCTGCCAACTTTTATCTACAAAATAAACTGATTGGGTA 1257
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 256 GCAAGTGAATGTAATAAATGTTAGCTTAACCTTTATGATCAAAACATCTGCTGTTTGA 197

QY 1258 GCAGGTATTTGATACATGTTACTAGTTGTAATAAAAAAATTAACCTTCTGGCCTCAAGCTAAT 1317
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Db 196 GCAGGTACTGATACATGCTGAATGTTCTAAAAAATAACTTCTGCTGCTACAGCTARA 137
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1318 TTACTCTGAATCTGCTAAAAAATAATATATATG------ATTTCGGTAATTTTTRA 1368
      || || || || || || || || || || || || || || || || || || || || ||
Db 136 GTATATGCTGAAGCTACTTAAAAAGCATATAGCGCCAGTTCCACTTTTCGCAAAATTTT 77
      || || || || || || || || || || || || || || || || || || || || ||
Qy 1369 TCAATTTCCCTTATATGATTTCTTATTTATTTATATGATGA 1410
      || || || || || || || || || || || || || || || || || || || || ||
Db 76 TCAATGTCCTTAATATTTATTTCTTCTATTTGTTGATGA 35
      || || || || || || || || || || || || || || || || || || || || ||

RESULT 3
BQ135164/c 602 bp mRNA linear EST 22-APR-2002
LOCUS
DEFINITION
INIT1.4.B05.g1.A006.G5 trophont cDNA (INIT1) Ichthyophthirius
multifiliis cDNA, mRNA sequence.
ACCESSION
BQ135164
VERSION
KEYWORDS
SOURCE
BQ135164.1 GI:20261263
ORGANISM
Ichthyophthirius multifiliis.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE
1 (bases 1 to 602)
AUTHORS
Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
Dickerson,H., Lin,T.-L. and Pratt,L.H.
TITLE
An EST database for Ichthyophthirius multifiliis (G5 isolate)
JOURNAL
Unpublished (2002)
COMMENT
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude polyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: T7
High quality sequence start: 3
High quality sequence stop: 602
POLYA=Yes.

FEATURES
source
1. 602
/organism="Ichthyophthirius multifiliis"
/strain="G5"
/db_xref="taxon:5932"
/clone_lib="G5 trophont cDNA (INIT1)"
/note="Vector: pBluescript SK(-) from Lambda Zap II;
Site.1: EcoRI; Site.2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.
Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into Lambda Zap
II. Plasmid DNA for sequencing was prepared by mass
excision."
BASE COUNT 214 a 103 c 92 g 193 t
ORIGIN
Query Match 14.0%; Score 198; DB 14; Length 602;
Best Local Similarity 66.4%; Pred. No. 3.8e-32;
Matches 352; Conservative 0; Mismatches 160; Indels 18; Gaps 4;

Qy 893 CAGTGGTCCCTACTTTAGCCAATAATGTAATATTCATGCCCTGATGCTACTGCA 952
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Db 599 CAGGTCTTGAGGCTAATTTAGCGCATATATGGCCATGAATGCTCCTGCTGCACTTTG 540
      || || || || || || || || || || || || || || || || || || || || ||
Qy 953 TTGCTAGTGGAGCAA---CTAATTATGTAATATATAAACAAGTCTCAAATTTGCTG 1009
      || || || || || || || || || || || || || || || || || || || || ||
Db 539 TTACACACGGATACACCTACTTATCTGTCATCTCTCATAAATGTGTAATTGTAAG 480
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Qy 1010 CTAACCTTTTATTTGATGTAATAATTTCTAGGCAGGAAGTAGTAGATGCAAGCATGTC 1069
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Db 479 CTGGCTTTTACTAAAA---TAGTAATTTTCAAGCAGGTAAAGTTTAATGCAATAAGTGTG 423
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1070 CAGCAATAAAGTTTAAAGCGCTGTAGCAACTGCGAGGTGGTACTCTACTTTAATTTGCAT 1129
      ||||| ||||| || || || || || || || || || || || || || || || || ||
Db 422 CAGTAAGTAAAACT---GGTTTCAGCATCTGTTCCAGGTAATAGTGTACTTTCAGCCACAT 366
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1130 AATGTCGCCCTTCAATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1189
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 365 AATGTTAAACGATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 306
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1190 AATAAGCAGCATCTGAATGTTGTAATGTTGCTGCCAACTTTTATATCTACAAAATAAAGTGT 1249
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 305 TAGCTTTAGCAAGTGAATGTAATAATGTTAGGCTAACTTTTATGCATCAAAAACATCTG 246
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1250 ATTGGGTAGCAGGTATTCATACATCTACTAGTGTGTAATAAANAATTAATCTTCTGGCGGTG 1309
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Db 245 GTTTTTCGACAGGCTACTGATACATCTACTGAATGTTCTTAAANAATTAATCTTCTGGTGCTA 186
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1310 AAGCTAAATTTACCTGCAATCTGCTAAAAAATAATATATATGCTG-----ATTTCGCTA 1360
      ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 185 CAGCTAAGATATATGCTGAAGCTACTTAAAGCATAATGCGCCAGTTCCACTTTTCGCA 126
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1361 ATTTTATCAATTTCCCTTATTTATTTGATTTCTTATTTATTTATGATGA 1410
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 125 AATTTTATCAATGCTTCAATATATTTATTTCTTCTTATTTGTTGATGA 76
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RESULT 4
BQ135179/c 590 bp mRNA linear EST 22-APR-2002
LOCUS
DEFINITION
INIT1.4.C08.g1.A006.G5 trophont cDNA (INIT1) Ichthyophthirius
multifiliis cDNA, mRNA sequence.
ACCESSION
BQ135179
VERSION
KEYWORDS
BQ135179.1 GI:20261278
SOURCE
EST.
ORGANISM
Ichthyophthirius multifiliis.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE
1 (bases 1 to 590)
AUTHORS
Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
Dickerson,H., Lin,T.-L. and Pratt,L.H.
TITLE
An EST database for Ichthyophthirius multifiliis (G5 isolate)
JOURNAL
Unpublished (2002)
COMMENT
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude polyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: T7
High quality sequence start: 43
High quality sequence stop: 590
POLYA=No.

FEATURES
source
1. 590
/organism="Ichthyophthirius multifiliis"
/strain="G5"
/db_xref="taxon:5932"
/clone_lib="G5 trophont cDNA (INIT1)"
/note="Vector: pBluescript SK(-) from Lambda Zap II;
Site.1: EcoRI; Site.2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.
Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into Lambda Zap
II. Plasmid DNA for sequencing was prepared by mass
excision."
BASE COUNT 207 a 103 c 94 g 186 t
ORIGIN

```

Query Match		14.0%;	Score 197;	DB 14;	Length 590;		
Best Local Similarity		66.4%;	Pred. No. 6.3e-32;				
Matches 351;		Conservative 0;	Mismatches 160;	Indels 18;	Gaps 4;		
QY	894	AGGTGGTGGCGCTACTTTAGCCAAATAAATGTAATATTCGATGCGCCCTGATGGTACTGCAAT	953				
DB	590	AGGTCTTGAGGCTAATTTAGCGCATAATGTGGCACTGAATGCTCTGCTGGCACTCTTGT	531				
QY	954	TGCTAGTCGAGCAA--CTAATATGTAATATTAACAGAAATGTCTAAATTTGGCTGC	1010				
DB	530	TACAGACGAGTACACCTACTTATCTACTGTATCACHCTCATANTGTGTAATTTGAAGC	471				
QY	1011	TAACTTTTATTTTGTGATGTAATAATTTCTAGCAGGAAGTAGTAGATCAAGCATGTCC	1070				
DB	470	TGGCTTTTACTAAAA--TAGTAATTTCGAAGCAGCTAAAAAGTTAATGCAATAAGTGTC	414				
QY	1071	AGCAATAAAGTTTAAAGCGCTGTAGCAACTGCAGGTGGTACTGTCTACTTTAATTTGCATA	1130				
DB	413	AGTAAGTAAAACT--GGTTCAGCATCTGTTCAGGTAATAGTGCTACTTCAGCCACATA	357				
QY	1131	ATGTGCGCTTGAATGCCCTGCTGGTACTGTACCGATGGAACAACATCTACTTTATAA	1190				
DB	356	ATGTTTAAACGATTCGCCCTGCTGGTACAGTGGTTGATGATGGTACATCAACTAATTTGT	297				
QY	1191	ATAAGCAGCATCTGAATGTGTTAAATGTCTGCCAACTTTTATATACTACAAAATAAAGCTGA	1250				
DB	296	AGCTTTAGCAAGTGAATGACTAAATGTTAGGCTAACTTTTATGATCATCAAAAACATCTGG	237				
QY	1251	TTGGGTAGCAGGTATGTATACATGACTAGTGTGTAATAAATAAATAACTTCGGCGCTGA	1310				
DB	236	TTTTGCGCAGGCTACTGATACATGACTGAATGTCTTAAAAAATAAATCTCTGGTGCTAC	177				
QY	1311	ACGTAATTTACCTGAATCTGCTAAAAAATAATATAATGTG-----ATTTCGCTAA	1361				
DB	176	AGCTAAGTATATGCTGAAGCTACTTAAAGACATAATGCGCGAGTTCACCTTTCGCANA	117				
QY	1362	TTTTTTATCAATTCCTTATTTATGATTTCTTATTTATTTATTTATGATGA	1410				
DB	116	ATTTTATCAATGCTCTTAATATTTATTTCTTCTATTTGTTGTGATGA	68				
RESULT 5							
BQ134889/c							
LOCUS							
DEFINITION						502 bp mRNA linear EST 22-APR-2002	
						INIT1_L_D07.b1.A006 G5 trophont cDNA (INIT1) Ichthyophthirius	
						multifiliis cDNA, mRNA sequence.	
ACCESSION						BQ134889	
VERSION						BQ134889.1 GI:20260988	
KEYWORDS						EST.	
SOURCE						Ichthyophthirius multifiliis.	
ORGANISM						Ichthyophthirius multifiliis.	
REFERENCE						Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;	
AUTHORS						Hymenostomatida; Ophryoglenina; Ichthyophthirius.	
						1 (bases 1 to 502)	
						Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,	
						Dickerson,H., Lin,T.-L. and Pratt,L.H.	
TITLE						An EST database for Ichthyophthirius multifiliis (G5 isolate)	
JOURNAL						Unpublished (2002)	
COMMENT						Contact: Cordonnier-Pratt MM	
						Laboratory for Genomics and Bioinformatics	
						The University of Georgia, Department of Plant Biology	
						Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA	
						Tel: 706 542 1860	
						Fax: 706 583 0210	
						Email: mmpratt@uga.edu	
						Sequences have been trimmed to exclude PolyA, vector, and regions	
						below Phred quality 16. The threshold for highest quality sequence	
						is 20.	
						Seq primer: JEN REV	
						High quality sequence stop: 474	
FEATURES						POLYA=Yes.	
						Location/Qualifiers	

source	1. .502					
	/organism="Ichthyophthirius multifiliis"					
	/strain="G5"					
	/db_xref="taxon:5932"					
	/clone_lib="G5 trophont cDNA (INIT1)"					
	/notes="Vector: pBluescript SK(-) from Lambda Zap II; Site_1: EcoRI; Site_2: EcoRI; The library was made from trophont polyA+ RNA of the G5 parasite strain. Double-stranded cDNA was linked to EcoRI adaptors, size fractionated, and material >500 bp cloned into lambda Zap II. Plasmid DNA for sequencing was prepared by mass excision."					
BASE COUNT	185 a	80 c	70 g	167 t		
ORIGIN						
Query Match	12.1%;	Score 171;	DB 14;	Length 502;		
Best Local Similarity	67.5%;	Pred. No. 2.2e-26;				
Matches 291;	Conservative 0;	Mismatches 125;	Indels 15;	Gaps 3;		
QY	989	CAGAATGCTAAATGTGCTGAACCTTTTATTTTGTATGTAATAATTTCTAGGCAGGAA	1048			
Ddb	498	CATAATGTGTTAATGTAAAGCTGGCTTTTACT---AAAATAGTAATTTTCGAAGCAGGTA	442			
QY	1049	GTAGTAGATCAAGACATGTCACCAATAAAGTTTAAAGCGCTGTAGCAACTGCAGGTG	1108			
Ddb	441	AAAGTTAATGCAATAAGTGTGCAGTAAGTAAACT--GTTTCAGCATCTGTTCCAGGTA	385			
QY	1109	GTACTGCTACTTTAATTTGCATAATGTGCCCTTGAAATGCCCTGCTGGTACTCTACTCACCG	1168			
Ddb	384	ATAGTGCTACTTTCAGCACATAATGTTAAACGATTCGCCCTGCTGGTACAGTGGTTGATG	325			
QY	1169	ATGGAACAACATCTACTTATAATAAGCAGCATCTGAATGTGTTAAATGTCTGCCAAT	1228			
Ddb	324	ATGGTACATCACTAAATTTTGTAGCTTTAGCAAGTGAATGACTAAATGTTAGGCTAACT	265			
QY	1229	TTTATACTACAAATAAAGTGAATGGGTAGCAGTATTGATACATGACTAGTTGTAATA	1288			
Ddb	264	TTTATGATCAAAACATCTGGTTTTCGACGAGGACTGATACATGACTGAAATGTTCTA	205			
QY	1289	AAAAATTAACCTTCGGCGCTGAAGCTAATTTAGCTGAATCTGCTAAAAAATAATAAT	1348			
Ddb	204	AAAAATTAACCTTCGGTCTACAGCTAAAGTATATGCTGAAGCTACTTAAAAAGCATAAT	145			
QY	1349	GTG-----ATTTCGCTAAATTTTATCAATTTCTTTATTTATTTGATTTCTTATATT	1399			
Ddb	144	GCGCCAGTTCACCTTCGCAAAATTTTATCAATGCTCTTAATATTATTCTTCTTATT	85			
QY	1400	TATTATGATGA	1410			
Ddb	84	TGTTGTGATGA	74			
RESULT 6						
BQ134871/c	445 bp mRNA linear EST 22-APR-2002					
LOCUS	INIT1_L_805.b1.A006 G5 trophont cDNA (INIT1) Ichthyophthirius multifiliis cDNA, mRNA sequence.					
DEFINITION						
ACCESSION	BQ134871					
VERSION	BQ134871.1 GI:20260970					
KEYWORDS	EST.					
SOURCE	Ichthyophthirius multifiliis.					
ORGANISM	Ichthyophthirius multifiliis					
REFERENCE	Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Ophryoglenina; Ichthyophthirius.					
AUTHORS	Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A., Dickerson,H., Lin,T.-L. and Pratt,L.H.					
TITLE	An EST database for Ichthyophthirius multifiliis (G5 isolate)					
JOURNAL	Unpublished (2002)					
COMMENT	Contact: Cordonnier-Pratt MM Laboratory for Genomics and Bioinformatics The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm 2502, Athens, GA 30602-7271, USA Tel: 706 542 1860 Fax: 706 583 0210 Email: mmpratt@uga.edu Sequences have been trimmed to exclude PolyA, vector, and regions below Phred quality 16. The threshold for highest quality sequence is 20. Seq primer: JEN REV High quality sequence stop: 474 POLYA=yes.					

Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmpratt@uga.edu

Sequences have been trimmed to exclude PolyA, vector, and regions below Phred quality 16. The threshold for highest quality sequence is 20.

Seq primer: JEN REV  
High quality sequence start: 37  
High quality sequence stop: 443  
POLYA=Yes.

#### FEATURES

Location/Qualifiers  
1..445

/organism="Ichthyophthirius multifiliis"  
/strain="G5"

/db\_xref="taxon:5932"

/clone\_lib="G5 trophont cDNA (INIT1)"

/note="Vector: pBluescript SK(-) from Lambda Zap II; Site1: EcoRI; Site2: EcoRI; The library was made from trophont polyA+ RNA of the G5 parasite strain.

Double-stranded cDNA was linked to EcoRI adaptors, size fractionated, and material >500 bp cloned into lambda Zap II. Plasmid DNA for sequencing was prepared by mass excision."

BASE COUNT 155 a 79 c 71 g 140 t

Query Match 11.6%; Score 163; DB 14; Length 445;  
Best Local Similarity 66.4%; Pred. No. 1,1e-24;  
Matches 286; Conservative 0; Mismatches 130; Indels 15; Gaps 3;

QY 989 CAGATGCTAAATGCTGCTAACTTTATTTGATGCTAATAATTTCTAGGCAGGAA 1048  
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 442 CATAATGCTGTACTTGAAGCTGGCTTTACT---AAAATAGTAATTTTGAAGCAGGTA 386  
QY 1049 GTAGTAGATGCAAGCATCTCCAGCAATAAAGTTTAAGCGCTGTAGCAACTGCAGGTG 1108  
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 385 AAGGTTAATGCAATAAGTGTGAGTAAGTAAAACT---GGTTCAGCATCTGTCCAGGTA 329  
QY 1109 GTACTGCTACTTTAATGTCATATGTCCTTTGAATGCCCTGCTGTACTGTACTACCG 1168  
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 328 ATAGTCTACTTACGACCAATAATGTTAAACGATGGCTGCTGTACAGTGGTTGATG 269  
QY 1169 ATGGAACACATCTACTTTAATAATAGCAGCATCTGAATGTTTAAATGTGTGCCAACT 1228  
|| || || || || || || || || || || || || || || || || || || || || || || || ||  
Db 268 ATGGTTTCATCAACTAATTTTGTAGCTTTTACCAAGTGAATGTCCTAAATGTTAGGCTAACT 209  
QY 1229 TTTATACTACAAAATAAACTGATGGGTAGCAGGATTGATACATCTACTACTTCTAATA 1288  
|| || || || || || || || || || || || || || || || || || || || || || || || ||  
Db 208 TTTATGCAATCAAAACATCTGGTTTGCAGCAGGTAAGTATACATCTACTGAATGTTCTA 149  
QY 1289 AAAAATAACTTCTGGCGCTGAAGCTAATTTACCTGAATCTGCTAAAAAAAATATATAAT 1348  
|| || || || || || || || || || || || || || || || || || || || || || || || ||  
Db 148 AAAAATAACTTTTGTGCTACAGCTAAAGTATATGCTGAAGCTACTTAAAGCATAT 89  
QY 1349 GTG-----ATTTCGCTAATTTTATCAATTTCCCTTATATGATTTCTTATTAAT 1399  
|| || || || || || || || || || || || || || || || || || || || || || || || ||  
Db 88 GCGCCAGTTTCCACTTTTCGAAAATTTTATCAATGCTCTTAAATATATTTCTTCTATT 29  
QY 1400 TATTATGATGA 1410  
|| |||||  
Db 28 TCCCGTGATGA 18

RESULT 7  
BQ135036/c  
LOCUS BQ135036 419 bp mRNA linear EST 22-APR-2002  
DEFINITION INIT1.2.D10.g1.A006 G5 trophont cDNA (INIT1) Ichthyophthirius multifiliis cDNA, mRNA sequence.  
ACCESSION BQ135036  
VERSION BQ135036.1 GI:20261135  
KEYWORDS EST.  
SOURCE Ichthyophthirius multifiliis.  
ORGANISM Ichthyophthirius multifiliis

#### REFERENCE

##### AUTHORS

##### TITLE

##### JOURNAL

##### COMMENT

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Ophryoglenina; Ichthyophthirius.

1 (bases 1 to 419)  
Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A., Dickerson,H., Lin,T.-L. and Pratt,L.H.  
An EST database for Ichthyophthirius multifiliis (G5 isolate)

Unpublished (2002)  
Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmpratt@uga.edu

Sequences have been trimmed to exclude PolyA, vector, and regions below Phred quality 16. The threshold for highest quality sequence is 20.

Seq primer: T7  
High quality sequence start: 306  
High quality sequence stop: 419  
POLYA=Yes.

#### FEATURES

Location/Qualifiers  
1..419

/organism="Ichthyophthirius multifiliis"

/strain="G5"

/db\_xref="taxon:5932"

/clone\_lib="G5 trophont cDNA (INIT1)"

/note="Vector: pBluescript SK(-) from Lambda Zap II; Site1: EcoRI; Site2: EcoRI; The library was made from trophont polyA+ RNA of the G5 parasite strain.

Double-stranded cDNA was linked to EcoRI adaptors, size fractionated, and material >500 bp cloned into lambda Zap II. Plasmid DNA for sequencing was prepared by mass excision."

BASE COUNT 140 a 74 c 73 g 132 t

Query Match 11.1%; Score 156.8; DB 14; Length 419;  
Best Local Similarity 66.8%; Pred. No. 2.4e-23;  
Matches 259; Conservative 0; Mismatches 117; Indels 12; Gaps 2;

QY 1032 TAATTTCTAGCAGGAAGTAGTAGTCAAAAGCATGTCCAGCAATAAAGTTTAAAGCGC 1091  
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 411 TAATTTCTGAAGCAGGTAAGGCTAATGCAACAAGTGTGACAGTAAGTAAACT---GGTTC 355  
QY 1092 TGTAGCAACTGCAGGTGGTACTGTCTACTTTTAATTTGCATAATGTCGCCCTTGAATGCCCTGC 1151  
|| || || || || || || || || || || || || || || || || || || || || || || || ||  
Db 354 AGCATCTGTTCCAGGTAATAGTGTCTACTTTCAGCCACATAATGTTTAAACAGATTGCCCTGC 295  
QY 1152 TGGTACTGTACTCACCAGTGAACAACATCTACTTATAATAAGCAGCATCTGAATCTGT 1211  
|| ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 294 TGGTACAGTGGTTGATGATGTGATCACTCACTAATTTTGTAGCTTTAGCAAGTGAATGTAC 235  
QY 1212 TAAATGTGTCGCCAACTTTTATACATAAAATAAAGTATGGGTAGCAGGTATTTGATAC 1271  
|| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 234 TAAATGTAGGCTAACTTTTATGATCAAAAACATCTGGTTTCGACAGGACTGATGATCC 175  
QY 1272 ATGTACTAGTTGTAATAAAAATTAACCTTGGCGCTGAAGCTAATTTACTGATGATCC 1331  
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 174 ATGTACTGAATGTTTAAAAAATTAACCTTGGGTGTACAGCTAAAGTATACGCGGAAGC 115  
QY 1332 TAAAAAAAATATAATATGTG-----ATTTCGCTAATTTTATCAATTTCTCTTATT 1382  
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 114 TACTTAAAGCATAAATGCGCCAGTTCCTCACTTTTCGAAAATTTTATCAATGCCCTTAAT 55  
QY 1383 ATTGATTTCTTATTTATTTATTTATGATGA 1410  
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 54 ATTTATTTCTTCTTATTTTGTGTGATGA 27

RESULT 8  
BQ135196/c  
LOCUS BQ135196 675 bp mRNA linear EST 22-APR-2002

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DEFINITION  INIT1_4_E06.g1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
              multifiliis cDNA, mRNA sequence.
ACCESSION  BQ135196
VERSION    BQ135196.1 GI:20261295
KEYWORDS   EST.
SOURCE     Ichthyophthirius multifiliis.
           Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
           Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE  1 (bases 1 to 675)
AUTHORS   Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
           Dickerson,H., Lin,T.-L. and Pratt,L.H.
TITLE     An EST database for Ichthyophthirius multifiliis (G5 isolate)
JOURNAL   Unpublished (2002)
COMMENT   Contact: Cordonnier-Pratt MM
           Laboratory for Genomics and Bioinformatics
           The University of Georgia, Department of Plant Biology
           Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
           Tel: 706 542 1860
           Fax: 706 583 0210
           Email: mmpratt@uga.edu
           Sequences have been trimmed to exclude polyA, vector, and regions
           below Phred quality 16. The threshold for highest quality sequence
           is 20.
           Seq primer: T7
           High quality sequence start: 42
           High quality sequence stop: 675
POLYA=No. Location/Qualifiers
           1..675
           /organism="Ichthyophthirius multifiliis"
           /strain="G5"
           /db_xref="taxon:5932"
           /clone_lib="G5 trophont cDNA (INIT1)"
           /note="Vector: pBluescript SK(-) from Lambda Zap II;
           Site_1: EcoRI; Site_2: EcoRI; The library was made from
           trophont polyA+ RNA of the G5 parasite strain.
           Double-stranded cDNA was linked to EcoRI adaptors, size
           fractionated, and material >500 bp cloned into lambda ZAP
           II. Plasmid DNA for sequencing was prepared by mass
           excision."
BASE COUNT  216 a 126 g 127 g 206 t
ORIGIN
Query Match          9.5%; Score 134.4; DB 14; Length 675;
Best Local Similarity 63.3%; Pred. No. 1.4e-18;
Matches 291; Conservative 0; Mismatches 156; Indels 13; Gaps 5;

QY  819  TCCTAATTTCAATCCAGGTAATAGTACATGCTTACCTTGCCCGCAATAAAGATTATGG 878
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  459  TCCTATGGTTCCTGGCCCTAATAGTAAATGCTAGCTTGCGAATCAAAAAGACCAA--- 403

QY  879  TGTCTGAAGCCATCGCAGTGGTGGCGCTACTTTAGCCCAATAATTAATATTCGATGCC 938
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  402  TTCTTAATCCAGATCAGGTCCTTGAGGCTAATTTAGCCGCAATAATGTGGCAGTAATGCC 343

QY  939  TGATGTACTGCAATTCGTAGTGGAG---CAACTAATATGTAATTAATAACAGAAATG 995
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  342  TGTCTGCACCTCTGTTACAGACGGAGTACACCTACTTATATCTGATCCTCATATG 283

QY  996  TCTAAATGTGCTGCTAACTTTTATTTTGGATGCTTAATAATTTCTAGGACGAAGTAGTAG 1055
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  282  TGTTAATTTGAAAGCTGGCTTTTACT---AAAATAGTAAATTTTCGAAGCAGGTAAGGTA 226

QY  1056  ATCCAAGCATGTCACAGCAATAAAGTTTAAAGCGCTGTFAGCACTGCAGGTGGTACTGC 1115
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  225  ATGCAATAAGTGGCAGTAGTAAGTAAACT---GGTTCAGCATCTGTTCCAGGTAATAGTGC 169

QY  1116  TACTTTTAATTCGATAATGTGCCCTTGAATGCCCTGCTGCTACTGTACTACACGATGGAAC 1175
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  168  TACTTCAGGCACATAATGTTAAAACGATGGCCCTGCTGCTGACAGTGGTGTATGATGGTAC 109

QY  1176  AACATCTACTTATAAATAGCAGCATCTGAATGTGTTAATGTGCTGCCAACTTTTATAC 1235

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Db  108  ATCAACTAATTTTGTAGCTTTAGCAAGTGAATGACTAATGTTAGGCTAACTTTTATGC 49
      || ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY  1236  TACAATAAAGTGAATGGGTAG-CAGGTATTGATACATG 1274
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  48  ATCAAAAACATCTGGTTTGCACCCAGGTACTGATACAG 9
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9
BQ134821/C
LOCUS      BQ134821
DEFINITION INIT1_4_D09.bl_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
              multifiliis cDNA, mRNA sequence.
ACCESSION  BQ134821
VERSION    BQ134821.1 GI:20260920
KEYWORDS   EST.
SOURCE     Ichthyophthirius multifiliis.
           Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
           Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE  1 (bases 1 to 599)
AUTHORS   Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
           Dickerson,H., Lin,T.-L. and Pratt,L.H.
TITLE     An EST database for Ichthyophthirius multifiliis (G5 isolate)
JOURNAL   Unpublished (2002)
COMMENT   Contact: Cordonnier-Pratt MM
           Laboratory for Genomics and Bioinformatics
           The University of Georgia, Department of Plant Biology
           Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
           Tel: 706 542 1860
           Fax: 706 583 0210
           Email: mmpratt@uga.edu
           Sequences have been trimmed to exclude PolyA, vector, and regions
           below Phred quality 16. The threshold for highest quality sequence
           is 20.
           Seq primer: JEN REV
           High quality sequence stop: 506
POLYA=No. Location/Qualifiers
           1..599
           /organism="Ichthyophthirius multifiliis"
           /strain="G5"
           /db_xref="taxon:5932"
           /clone_lib="G5 trophont cDNA (INIT1)"
           /note="Vector: pBluescript SK(-) from Lambda Zap II;
           Site_1: EcoRI; Site_2: EcoRI; The library was made from
           trophont polyA+ RNA of the G5 parasite strain.
           Double-stranded cDNA was linked to EcoRI adaptors, size
           fractionated, and material >500 bp cloned into lambda ZAP
           II. Plasmid DNA for sequencing was prepared by mass
           excision."
BASE COUNT  191 a 113 c 111 g 183 t 1 others
ORIGIN
Query Match          9.1%; Score 127.8; DB 14; Length 599;
Best Local Similarity 62.8%; Pred. No. 3.6e-17;
Matches 268; Conservative 0; Mismatches 147; Indels 12; Gaps 4;

QY  819  TCCTAATTTCAATCCAGGTAATAGTACATGCTTACCTTGCCCGCAATAAAGATTATGG 878
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  431  TCCATGTTCTCTGCCCTAATAGTAAATGCTAGCTTGCGAATCAAAAAGACCAA--- 375

QY  879  TGCTGAAGCCACTGCAGGTGGTGGCGCTACTTTAGCCAAATAATGTAATATTGATGCC 938
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  374  TTCTTAATCCAGATCAGGTCTTTAGGCTAATTTAGCCGCAATAATGTGGCTAGTATGCC 315

QY  939  TGATGGTACTGCAATTCGTAGTGGAG---CAACTAATATGTAATATATAAAGAGAAATG 995
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  314  TGTCTGGCACTCTTGTACAGACGGAGTAACACCTACTTATCTACTGATCCTCATATG 255

QY  996  TCTAAATGTGCTGCTAACTTTTATTTTGTGATGGTAAATTTCTAGGACGAAGTAGTAG 1055
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  254  TGTTAATTTGTAAGCTGGCTTTTACT---AAAATAGTAAATTTTCGAAGCAGGTAAGGTA 198

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QY 1056 ATGCAAGCATGTCACCAATAAAGTTTAAAGCGCTGTAGCAACTGCAGGTGGTACTGTC 1115
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 197 ATGCAATAAGTGTGCAGTAAGTAAACT---GGTTGAGCATCTGTTCCAGGTAATAGTGC 141
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1116 TACTTTAATTTGCAATAATGTCCTTGAATGCCCTGCTGGTACGTACTACCGCATGGAAC 1175
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 140 TACTTCAGCCACATAATGTTAAACAGATTGCCCTGCTGGTACAGTGGTTGATGATGGTAC 81
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1176 ACATCTACTTANTAATAGCAGCATCTGAATGTGTTAAATGTCGTGCCAATCTTTTATAC 1235
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 80 ATCAACTAATTTTGTAGCTTTAGCAAGTGAATCTACTAAATGTTAGGCTAATCTTTTATGC 21
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1236 TACAAA 1242
      |||||
Db 20 ATCAAAA 14
      |||||

RESULT 10
BQ134879
LOCUS
DEFINITION
  INIT1_1_C04_b1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
  multifiliis cDNA, mRNA sequence.
ACCESSION
  BQ134879
VERSION
  BQ134879.1 GI:20260978
KEYWORDS
  EST.
SOURCE
  Ichthyophthirius multifiliis.
  Ichthyophthirius multifiliis.
  Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
  Hymenostomatida; Ophryoglenina; Ichthyophthirius.
  1 (bases 1 to 540)
  Dickerson,H., Lin,T.-L. and Pratt,L.H.
  Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
  An EST database for Ichthyophthirius multifiliis (G5 isolate)
  Unpublished (2002)
  Contact: Cordonnier-Pratt MM
  Laboratory for Genomics and Bioinformatics
  The University of Georgia, Department of Plant Biology
  Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
  Tel: 706 542 1860
  Fax: 706 583 0210
  Email: mmpratt@uga.edu
  Sequences have been trimmed to exclude PolyA, vector, and regions
  below Phred quality 16. The threshold for highest quality sequence
  is 20.
  Seq primer: JEN REV
  High quality sequence stop: 449
  POLYA-No.
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      /strain="G5"
      /db_xref="taxon:5932"
      /clone_lib="G5 trophont cDNA (INIT1)"
      /note="Vector: pBluescript SK(-) from Lambda Zap II;
      Site_1: EcoRI; Site_2: EcoRI; The library was made from
      trophont polyA+ RNA of the G5 parasite strain.
      Double-stranded cDNA was linked to EcoRI adaptors, size
      fractionated, and material >500 bp cloned into lambda Zap
      II. Plasmid DNA for sequencing was prepared by mass
      excision."
BASE COUNT 163 a 97 c 97 g 183 t
ORIGIN

Query Match 8.2%; Score 115.2; DB 14; Length 540;
Best Local Similarity 60.0%; Pred. No. 1.8e-14;
Matches 245; Conservative 0; Mismatches 133; Indels 30; Gaps 2;

QY 1 ATGAAAAATAATTTAGTAAATATTTGATTTTATTTATTTATTTATTTATTTATTTAAATCT 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 33 ATGAAATTTAATATTTTAAATATTTTGTATTTTCTTTATTTATTTATTTATTTAGAGCT 92
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 GCTAATTCCTGCTGGAACTGAACACTAACACAGCCGGATAAGTTGATGATCTAGGAAC 120
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Db 93 GTTAATTTGCTCTAATTTGGTCTGCAATTTGCAATGCAATAATCTGATACAGGAGCTGCAGAT 152
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 CCTGCAAAATTTGTTAATTTAGTAAACACTTTTATTATATATAATGCTGCTGCT----- 174
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 153 ATAAATACTTGTACTCAITTTGCTAAAAACACTTTTACTTTAATGGTGGTAATCCCTGCAGGT 212
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 175 -----TTTCGTTCTCTGCTGTAGTGTACCTGTACACCTTTGTCCATAA 213
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 213 CAGGCTCCTGGTGTACAATTTCAATCCAGGTGTTAGTCAGTCAGTCATGCTGCCAAGTA 272
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 214 AAAAAAGATGCTGGTGTACCAATCCACTGCTACTGCTAAATTTAGTCACATAATGT 273
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 273 CACAAA---GCGGATTTCTCAACACAGATAAGTGTGTATGCTAAATTTAGCGGCATAATGT 329
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 274 AACGTTAAATGCCCTGCTGCTACCGCAATTTGAGGTGAGCAACAGATTATTCAGCAANTA 333
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 330 AGCAACTTATGTCCTGCTGGCACTGCAAGTGAAGATGATCACCCTTACTTTACTTAATCC 389
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 334 ATCAGAGAATGTTTAAATTTAGTAATTAATTTTATAATGAAATGCT 381
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 390 CTCACATAATGTTAATTTGTAACCTAACTTTTACTTTAATGGTGGT 437
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RESULT 11
BQ134810
LOCUS
DEFINITION
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  INIT1_4_C08_b1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
  multifiliis cDNA, mRNA sequence.
ACCESSION
  BQ134810
VERSION
  BQ134810.1 GI:20260909
KEYWORDS
  EST.
SOURCE
  Ichthyophthirius multifiliis.
  Ichthyophthirius multifiliis.
  Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
  Hymenostomatida; Ophryoglenina; Ichthyophthirius.
  1 (bases 1 to 538)
  Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
  Dickerson,H., Lin,T.-L. and Pratt,L.H.
  An EST database for Ichthyophthirius multifiliis (G5 isolate)
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  Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
  Tel: 706 542 1860
  Fax: 706 583 0210
  Email: mmpratt@uga.edu
  Sequences have been trimmed to exclude PolyA, vector, and regions
  below Phred quality 16. The threshold for highest quality sequence
  is 20.
  Seq primer: JEN REV
  High quality sequence stop: 531
  POLYA-No.
  Location/Qualifiers
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      /strain="G5"
      /db_xref="taxon:5932"
      /clone_lib="G5 trophont cDNA (INIT1)"
      /note="Vector: pBluescript SK(-) from Lambda Zap II;
      Site_1: EcoRI; Site_2: EcoRI; The library was made from
      trophont polyA+ RNA of the G5 parasite strain.
      Double-stranded cDNA was linked to EcoRI adaptors, size
      fractionated, and material >500 bp cloned into lambda Zap
      II. Plasmid DNA for sequencing was prepared by mass
      excision."
BASE COUNT 155 a 101 c 106 g 175 t
ORIGIN

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Query Match 8.1%; Score 113.8; DB 14; Length 538;
Best Local Similarity 59.2%; Pred. No. 3.5e-14;
Matches 234; Conservative 0; Mismatches 152; Indels 9; Gaps 2;

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QY	171	TGCTTTCCGTTCTGGTCTAGTACGTTACACCTTGTCCTCAATAAAAAAGATGCTGGTGC	230
DB	149	TCCTATGGTTCTGGCCCTAATAGTAATCGTAGCTTGCGAATCAAAAAAGACCAATTC	208
QY	231	TTAACCAAAATCCACCTGCTACTGCTAATATTAGTCACATAATGTAACGTTAAATGCCCTGC	290
DB	209	TTAATCCAGATCAGGCTTTCAGGCGTAATTTAGCCGCAATATGTGGCACTCAATGTCTCTGC	268
QY	291	TGGTACCAGCAATTCGACGTTGAGCAACA---GATTATGCAGCAATAATACAGAAATGCT	347
DB	269	TGGCAGCTCTGTTACAGACGGAGTAACACCTACTTATCTATCTATCTCATAAATGCT	328
QY	348	TAATTTGTAGAATTAATTTTATATGAAAATGCTCCAAATTTTAAATCGAGGTGCTAGTAC	407
DB	329	TAATTTGTAAGCTGGCTTTTACTAAATAGT-----AATTTCAAGCAGGTAAAGTTA	382
QY	408	ATGCACAGCTTGCCGGTAACACAGAGTGGTGGTGCAATGACTCTGGTAATGCCGCTAC	467
DB	383	ATGCAATAAGTGTGCAGTAAGTAAACATGGTTACGACATCTGTTCCAGGTAATAGTGTCTAC	442
QY	468	CATAGTCGCAATAATGTAACGTCGATGCTCCCTACCTGCTACTGCACTTGTATGATGAGTAAC	527
DB	443	TTACGCCACATAATGTTAAACAGATTGCCCTGCTGGTACAGTGGTTGATGATGATGATCATC	502
QY	528	TACTGATTATGTTAGATCAATTCACAGATGCTGTTA	562
DB	503	AACATAATTTTGTAGCTTTAGCAAGTGAATGACTA	537
RESULT 12			
BQ134905			
LOCUS	INIT1_L1_F04.b1_A006	G5 trophont cDNA (INIT1) Ichthyophthirius	linear EST 22-APR-2002
DEFINITION	multifiliis cDNA, mRNA sequence.		
ACCESSION	BQ134905		
VERSION	BQ134905.1	GI:20261004	
KEYWORDS	EST.		
SOURCE	Ichthyophthirius multifiliis.		
ORGANISM	Ichthyophthirius multifiliis.		
REFERENCE	Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Ophryoglenina; Ichthyophthirius.		
AUTHORS	Clark, T., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A., Dickerson, H., Lin, T.-L. and Pratt, L.H.		
TITLE	An EST database for Ichthyophthirius multifiliis (G5 isolate)		
COMMENT	Contact: Cordonnier-Pratt MM Laboratory for Genomics and Bioinformatics The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA Tel: 706 542 1860 Fax: 706 583 0210 Email: mmpratt@uga.edu Sequences have been trimmed to exclude polyA, vector, and regions below Phred quality 16. The threshold for highest quality sequence is 20. Seq primer: JEN REV High quality sequence stop: 629 POLYA-No.		
FEATURES	Location/Qualifiers		
source	1..630	/organism="Ichthyophthirius multifiliis"	
		/strain="G5"	
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		/note="Vector: pBluescript SK(-) from Lambda Zap II; Site 1: EcoRI; Site 2: EcoRI; The library was made from trophont polyA+ RNA of the G5 parasite strain. Double-stranded cDNA was linked to EcoRI adaptors, size fractionated, and material >500 bp cloned into lambda Zap II. Plasmid DNA for sequencing was prepared by mass excision."	





